

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 19:31:38 ; Search time 4930.81 Seconds

(without alignments)
17544.846 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 cttecaaggccccccatgaaaaaaaaaaaaaaatggtagagagatatttc 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 799276

Minimum DB seq length: 15
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb.ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_on:*
 5: gb_ov:*
 6: gb_bt:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_v1:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pi:*
 26: em_roi:*
 27: em_sts:*
 28: em_un:*
 29: em_v1:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_inv:*

ALIGNMENTS

RESULT

1

AX099610/c AX099610

LOCUS Sequence 250 from Patent WO0119988. 29 bp DNA

DEFINITION Sequence 250 from Patent WO0119988. linear PAT 02-APR-2001

ACCESSION AX099610

VERSION 1 GI:13538665

KEYWORDS synthetic construct.

SOURCE artificial sequence.

ORGANISM (bases 1 to 29)

REFERENCE Jacobs, K., McCoy, J. M., Lavallie, E. R., Collins-Racie, L. A., Evans, C.,

AUTHORS Merberg, D., Treacy, M., Bowman, M. R., Spaulding, V. and Agostino, M. J.

TITLE Secreted proteins and polynucleotides encoding them

JOURNAL Patent: WO 0119988-A 250 22-MAR-2001; Genetics Institute, Inc. (US)

FEATURES Location/Qualifiers

source 1..29

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="oligonucleotide"

/note="biotinylated phosphoramidite residue"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

%

Match

Length

DB

ID

BASE COUNT 7 a 9 c 4 g 8 t 1 others
ORIGIN

Query Match 0.7%; Score 28; DB 6; Length 29;
Best Local Similarity 96.6%; Pred. No. 2.9e+04;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
VERSION 75 aagaatcattcgtgtcgatctcaccag 103
Db 29 AAGGAATTCGTCGACCTCAGCNG 1

RESULT 2
ROTVP7AK
LOCUS ROTVP7AK
DEFINITION Homo sapiens rotavirus 2 (strain 2743) outer capsid protein (vp7)
RNAME partial cds.
ACCESSION M37350
VERSION M7350.1 GI:548269
KEYWORDS VP7 gene; outer capsid protein.
SOURCE Human rotavirus 2 (strain 2743) RNA.
ORGANISM Viruses; dsRNA viruses; Reoviridae; Rotavirus.
REFERENCE 1. (bases 1 to 87)
AUTHORS Green,K.Y., Sears,J.F., Taniguchi,K., Midtun,K., Hoshino,Y., Gorzilja,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.
TITLE Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene
JOURNAL J. Virol. 62, 1819-1823 (1988)
MEDLINE 88188272
FEATURES Source

BASE COUNT 32 a 11 c 22 g 22 t
ORIGIN

Query Match 0.7%; Score 27.2; DB 14; Length 87;
Best Local Similarity 61.1%; Pred. No. 5.2e-04;
Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
VERSION 818 ctgtqaaggtagtttcgtggatgaatggactatgtctaatttgtgaca 877
Db 8 CTAATAATGAGATTTCAGAAGATGATGAAATACTAAACTACGGACGTGACTACAT 67
QY 878 ctgggtttatg 889
/db_xref="GI:548271"
/ab_xref="taxon:36429"
1. .87
<1. .>87
/gene="VP7"
/gene="VP7"
<1. .>87
/codon_start=1
/product="outer capsid protein"
/protein_id="AAA47369.1"
/db_xref="GI:548269"
/translation="KAEKNETSDDMENTKTIDVSTFEIASS"
BASE COUNT 32 a 11 c 22 g 22 t
ORIGIN

RESULT 4
AF213231
LOCUS AF213231
DEFINITION Bison bison clone 15.1.1 microsatellite BMS410-89.
ACCESSION AF213231
VERSION AF213231.1 GI:11837834
KEYWORDS SOURCE
ORGANISM American bison.
Bison bison
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bison.
REFERENCE 1. (bases 1 to 89)
AUTHORS Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE Validation of 15 microsatellites for parentage testing in North American bison, Bison bison and domestic cattle
JOURNAL Anim. Genet. 31 (6), 360-366 (2000)
MEDLINE 21070477
REFERENCE 2. (bases 1 to 89)
AUTHORS Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE Direct Submission
JOURNAL University, Bldg. 1197 Rm.226, College Station, TX 77843-4467, USA
FEATURES SOURCE
/organism="Bison bison"
/db_xref="taxon:9901"
/clone="15.1.1"
primer_bind 1. .89
repeat_region 1. .89
/note="microsatellite BMS410-89"
/rpt-type=tandem
primer_bind 70. .89

RESULT 3
ROTVPAL
LOCUS ROTVP7AL
DEFINITION Homo sapiens rotavirus 2 (strain 2899) outer capsid protein (vp7)
RNAME partial cds.
ACCESSION M37351
VERSION M37351.1 GI:548270
KEYWORDS VP7 gene; outer capsid protein.
SOURCE Human rotavirus 2 (strain 2899) RNA.
ORGANISM Human rotavirus 2 (strain 2899)

REFERENCE 1. (bases 1 to 87)
AUTHORS Green,K.Y., Sears,J.F., Taniguchi,K., Midtun,K., Hoshino,Y., Gorzilja,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.
TITLE Prediction of the VP7 protein gene analysis of the VP7 protein sequence
JOURNAL J. Virol. 62, 1819-1823 (1988)
MEDLINE 88188272
FEATURES SOURCE
/organism="Human rotavirus 2"
/strains="2899"
/db_xref="taxon:36429"
1. .87
<1. .>87
/gene="VP7"
/gene="VP7"
/codon_start=1
/product="outer capsid protein"
/protein_id="AAA47369.1"
/db_xref="GI:548271"
/translation="NEAKNEISDDEWENTKTIDVSTFEIASS"
BASE COUNT 11 c 22 g 22 t
ORIGIN

Query Match 0.7%; Score 27.2; DB 14; Length 87;
Best Local Similarity 61.1%; Pred. No. 5.2e-04;
Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
VERSION 818 ctgtqaaggtagtttcgtggatgaatggactatgtctaatttgtgaca 877
Db 8 CTAATAATGAGATTTCAGAAGATGATGAAATACTAAACTACGGACGTGACTACAT 67
QY 878 ctgggtttatg 889
/db_xref="GI:548269"
/ab_xref="GI:548270"
1. .87
/gene="VP7"
/gene="VP7"
<1. .>87
/codon_start=1
/product="outer capsid protein"
/protein_id="AAA47369.1"
/db_xref="GI:548269"
/translation="KAEKNETSDDMENTKTIDVSTFEIASS"
BASE COUNT 11 c 22 g 22 t
ORIGIN

RESULT 4
AF213231
LOCUS AF213231
DEFINITION Bison bison clone 15.1.1 microsatellite BMS410-89.
ACCESSION AF213231
VERSION AF213231.1 GI:11837834
KEYWORDS SOURCE
ORGANISM American bison.
Bison bison
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bison.
REFERENCE 1. (bases 1 to 89)
AUTHORS Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE Validation of 15 microsatellites for parentage testing in North American bison, Bison bison and domestic cattle
JOURNAL Anim. Genet. 31 (6), 360-366 (2000)
MEDLINE 21070477
REFERENCE 2. (bases 1 to 89)
AUTHORS Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE Direct Submission
JOURNAL University, Bldg. 1197 Rm.226, College Station, TX 77843-4467, USA
FEATURES SOURCE
/organism="Bison bison"
/db_xref="taxon:9901"
/clone="15.1.1"
primer_bind 1. .89
repeat_region 1. .89
/note="microsatellite BMS410-89"
/rpt-type=tandem
primer_bind 70. .89

	BASE COUNT	29 a	33 c	8 g	19 t
ORIGIN					
Query Match	0.6%	Score 25.8; DB 4;	Length 89;		
Best Local Similarity	56.5%	Pred. No. 1.3e+05;	Mismatches 37;	Indels 0;	Gaps 0;
Matches	48;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
DEFINITION	Homo sapiens rotavirus 2 (strain HN126) outer capsid protein (VP7)				
ACCESSION	M37349				
VERSION	M37349.1	GI:548266			
KEYWORDS	VP7 gene; outer capsid Protein.				
SOURCE	Human rotavirus 2 (strain HN126) RNA.				
ORGANISM	Human rotavirus 2				
REFERENCE	1. (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y., Gorzilka,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J. Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene J. Virol. 62, 1819-1823 (1988)				
AUTHORS					
JOURNAL					
MEDLINE					
FEATURES					
source	Location/Qualifiers 1. .87 <organism="Human rotavirus 2"> <strain="C"> <db_xref="taxon:36429"> <gene="VP7"> <! .>87 </gene>"VP7" </codon_start=1 <product="outer capsid protein"> <protein_id="AA447371_1"> <db_xref="GI:548273"> </translation="AEAKNEISDDEWENKTDVNTFEIVASS"				
RESULT	5				
ROTVP7A	ROTVP7A	87 bp ss-RNA	linear	VRL 23-SEP-1994	
DEFINITION	Homo sapiens rotavirus 2 (strain HN126) outer capsid protein (VP7)				
ACCESSION	M37349				
VERSION	M37349.1	GI:548266			
KEYWORDS	VP7 gene; outer capsid Protein.				
SOURCE	Human rotavirus 2 (strain HN126) RNA.				
ORGANISM	Human rotavirus 2				
REFERENCE	1. (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y., Gorzilka,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J. Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene J. Virol. 62, 1819-1823 (1988)				
AUTHORS					
JOURNAL					
MEDLINE					
FEATURES					
source	Location/Qualifiers 1. .87 <organism="Human rotavirus 2"> <strain="C"> <db_xref="taxon:36429"> <gene="VP7"> <! .>87 </gene>"VP7" </codon_start=1 <product="outer capsid protein"> <protein_id="AA447371_1"> <db_xref="GI:548273"> </translation="AEAKNEISDDEWENKTDVNTFEIVASS"				
BASE COUNT	33 a				
ORIGIN					
RESULT	5				
ROTVP7A	ROTVP7A	87 bp ss-RNA	linear	VRL 23-SEP-1994	
DEFINITION	Homo sapiens rotavirus 2 (strain HN126) outer capsid protein (VP7)				
ACCESSION	M37349				
VERSION	M37349.1	GI:548266			
KEYWORDS	VP7 gene; outer capsid Protein.				
SOURCE	Human rotavirus 2 (strain HN126) RNA.				
ORGANISM	Human rotavirus 2				
REFERENCE	1. (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y., Gorzilka,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J. Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene J. Virol. 62, 1819-1823 (1988)				
AUTHORS					
JOURNAL					
MEDLINE					
FEATURES					
source	Location/Qualifiers 1. .87 <organism="Human rotavirus 2"> <strain="C"> <db_xref="taxon:36429"> <gene="VP7"> <! .>87 </gene>"VP7" </codon_start=1 <product="outer capsid protein"> <protein_id="AA447371_1"> <db_xref="GI:548273"> </translation="AEAKNEISDDEWENKTDVNTFEIVASS"				
BASE COUNT	34 a				
ORIGIN					
RESULT	7				
ROTVP7AN	ROTVP7AN	87 bp ss-RNA	linear	VRL 23-SEP-1994	
DEFINITION	Homo sapiens rotavirus 2 (strain V197) outer capsid protein (VP7)				
ACCESSION	M37353				
VERSION	M37353.1	GI:548274			
KEYWORDS	VP7 gene; outer capsid Protein.				
SOURCE	Human rotavirus 2 (strain V197) RNA.				
ORGANISM	Human rotavirus 2				
REFERENCE	1. (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y., Gorzilka,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J. Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene J. Virol. 62, 1819-1823 (1988)				
AUTHORS					
JOURNAL					
MEDLINE					
FEATURES					
source	Location/Qualifiers 1. .87 <organism="Human rotavirus 2"> <strain="V197"> <db_xref="taxon:36429"> <gene="VP7"> <! .>87 </gene>"VP7" </codon_start=1				
RESULT	6				
ROTVP7AM	ROTVP7AM	87 bp ss-RNA	linear	VRL 23-SEP-1994	
DEFINITION	Homo sapiens rotavirus 2 (strain C) outer capsid protein (VP7) RNA, partial cds.				
ACCESSION	M37352				

RESULT	9	Query Match	0.6%; Score 25; DB 6; Length 70;	Locus	AF272967
BASE COUNT	272967/c	/product="outer capsid protein"		/protein_id="MAM7372.1"	Mastacembelus aculeatus doublesex-like protein Dmrt2a gene, partial
ORIGIN		/db_xref="GI:548275"		/translation="AEAKNEHISDDEWENTKTDVNTFEIVASS"	
ACCESION				AF272967	
VERSION				AF272967.1	GI:10567711
KEYWORDS					
SOURCE					
ORGANISM					Mastacembelus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Synbranchiformes; Mastacembelidae; Mastacembelus.					
REFERENCE					
AUTHORS					Huang, X. and Zhou, R.
JOURNAL					J. Exp. Zool. (2002) In press
REFERENCE					2 (bases 1 to 94)
AUTHORS					Huang, X. and Zhou, R.
TITLE					Direct Submission
JOURNAL					Submitted (30-MAY-2000) Genetics, Wuhan University, Luojia, Wuhan, Hubei 430072, P.R. China
FEATURES					Location/Qualifiers
Source					1. .94
DEFINITION					/organism="Mastacembelus aculeatus"
LOCUS					/db_xref="taxon:138129"
ACCESSION					<1. .>94
VERSION					/product="doublesex-like protein Dmrt2a"
KEYWORDS					<1. .>94
SOURCE					/note="contains DM domain"
ORGANISM					/codon_start=2
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bison.					/product="doublesex-like protein Dmrt2a"
AUTHORS					/protein_id="AGI1852.1"
JOURNAL					/db_xref="GI:10567712"
REFERENCE					/translation="VVSCLKGHKRKRWRDCQCANCNLLVERQRY"
AUTHORS					
JOURNAL					
REFERENCE					
KEYWORDS					
FEATURES					
source					
BASE COUNT					
ORIGIN					
RESULT	13	Query Match	0.6%; Score 25.4; DB 5; Length 94;	LOCUS	AF272967
BASE COUNT	272967	Best Local Similarity	61.2%; Pred. No. 1.6e+05;	DEFINITION	Mastacembelus aculeatus doublesex-like protein Dmrt2a gene, partial
ORIGIN		Matches	41; Conservative	ACCESSION	AF272967
RESULT	10	Matches	0; Mismatches	VERSION	AF272967.1
BASE COUNT	171468	Indels	26; Indels	KEYWORDS	GI:3007603
ORIGIN		Gaps	0; Gaps	SOURCE	
RESULT	10	Organism	0; Gaps	ORGANISM	Unknown. Unclassified.
BASE COUNT	171468	Unclassified.		REFERENCE	1 (bases 1 to 70)
ORIGIN				AUTHORS	Buchwald,M., Stratheo,C.A., Wevrick,R. and Mathew,C.George.Porter.
RESULT	10			TITLE	Ranconi Anemia Type C gene
BASE COUNT	171468			JOURNAL	Patent: US 568192-A 9 28-Oct-1997;
ORIGIN				FEATURES	Location/Qualifiers
RESULT	10			Source	1. .70
BASE COUNT	26				/organism="unknown"
ORIGIN	a				
RESULT	9				
BASE COUNT	26				
ORIGIN	c				
RESULT	9				
BASE COUNT	26				
ORIGIN	t				

	DEFINITION
RESULT_11	Torrentophryne tuberospina KIZ-91A089 cytochrome b gene, partial
LOCUS	cds; mitochondrial gene for mitochondrial product.
DEFINITION	AF174510/c
VERSION	AF174510.1
KEYWORDS	Torrentophryne aspinia.
SOURCE	Mitochondrion Torrentophryne tuberospina
ORGANISM	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Torrentophryne.
REFERENCE	1 (bases 1 to 97)
AUTHORS	Liu,W., Lathrop,A., Fu,J. and Murphy,R.W.
JOURNAL	Phylogeny of East Asian bufonids inferred from mitochondrial DNA sequences (Anura: Amphibia)
MEDLINE	20179527
PUBLMED	10713847
REFERENCE	2 (bases 1 to 97)
AUTHORS	Liu,W., Lathrop,A., Fu,J. and Murphy,R.W.
JOURNAL	Submitted (26-JUN-1999) CBCB, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario M5S 2C6, Canada
FEATURES	Location/Qualifiers
source	<p>1..97 (bases 1 to 97) /organism="Torrentophryne aspinia" /organelle="mitochondrion" /specimen_voucher="KIZ-91A011" /db_xref="taxon:133606" /country="China: Yunnan, Yangbi Co." <1..>97 /product="cytochrome b" <1..>97 /codon_start=2 /transl_table=2 /product="cytochrome b" /protein_id="AAF64628.1" /obj_xref="GI:7620456" /translation="MIGOLASVSVFLIFITPLGLTENKLTLQ"</p>
BASE COUNT	29 a 30 c 8 g 30 t
ORIGIN	
Query Match	0.6%; Score 24.8; DB 5; Length 97;
Best Local Similarity	54.3%; Pred. No. 2.4e+05; Indels 0; Gaps 0;
Matches	50; Conservative 0; Mismatches 42; Gaps 0;
LOCUS	SYNDEL951
DEFINITION	X.laevis DNA containing insertion element Tn9, deleted element, 5'
VERSION	end.
KEYWORDS	
SRGNM	M10780.1 GI:203208
SOURCE	deletion; deletion mutant. 1 of 2
ORGANISM	X.laevis oocyte 5S DNA and transposon Tn9 DNA, combined in plasmid PMBR ⁺ , mutants 95 and 10.
REFERENCE	1 (bases 1 to 90)
AUTHORS	Fedoroff,N.V.
JOURNAL	Structure of deletion derivatives of a recombinant plasmid containing the transposable element Tn9 in the spacer sequence of Xenopus laevis 5S DNA
RESULT_12	
LOCUS	AF174510
BASE COUNT	97 bp
ORIGIN	linear
Query Match	0.6%; Score 24.8; DB 5; Length 97;
Best Local Similarity	54.3%; Pred. No. 2.4e+05; Indels 0; Gaps 0;
Matches	50; Conservative 0; Mismatches 42; Gaps 0;
LOCUS	SYNDEL951
DEFINITION	X.laevis DNA containing insertion element Tn9, deleted element, 5'
VERSION	end.
KEYWORDS	
SRGNM	M10780.1 GI:203208
SOURCE	deletion; deletion mutant. X.laevis oocyte 5S DNA and transposon Tn9 DNA, combined in plasmid PMBR ⁺ , mutants 95 and 10.
ORGANISM	synthetic construct artificial sequence.
REFERENCE	1 (bases 1 to 90)
AUTHORS	Fedoroff,N.V.
JOURNAL	Structure of deletion derivatives of a recombinant plasmid containing the transposable element Tn9 in the spacer sequence of Xenopus laevis 5S DNA

JOURNAL	Cold Spring Harb. Symp. Quant. Biol.	43,	1287-1292	(1979)
MEDLINE	80023367			
FEATURES	location/Qualifiers			
source	1. .90			
BASE COUNT	28 a 9 g 9 c 8 g 45 t			
ORIGIN	/db_xref="taxon:32630"			
RESULT	14			
LOCUS	ttaacagcacatgaatttaggccttggtanattggaaatccgtggccaaacaagac	0.6%	Score 24.6; DB 12;	Length 90;
DEFINITION	Best Local Similarity 55.2%; Pred. No. 2.7e+05; Mismatches 48; Conservative 0; Indels 0; Gaps 0;			
ACCESSION	3148			
VERSION	90			
KEYWORDS	TGAAACTTGAAAAATTAACTTGAAAATCAACCTTGAAACGT			
SOURCE	TGAAACTTGAAAAATTAACTTGAAACGT			
ORGANISM	Db			
REFERENCE	3175			
AUTHORS	QY 3149 ggtggactttaaaaattttaaattca			
TITLE	Db 30 TGAAACTTGAAAAATTAACTTGAAACGT			
JOURNAL	4			
MEDLINE	91310603			
REMARK	GenBank Staff at the National Library of Medicine created this entry [NCBI gibsg 45981] from the original journal article. This sequence comes from seq 5a. On Nov 21, 1996 this sequence version replaced gi:1619721. *ERRATUM*, Vol. 173, no. 6, p. 2097.			
COMMENT				
FEATURES	gene			
source	AF326227			
BASE COUNT	27 a 14 c 24 g 21 t			
ORIGIN	/gene="Selenoprotein A"			
RESULT	1			
LOCUS	AF326227	70 bp	DNA	linear
DEFINITION	Arabidopsis thaliana small nucleolar RNA R83, complete sequence.			
ACCESSION	AF326227			
VERSION	1			
KEYWORDS	GRN			
SOURCE	AF326227.1 GT:13183695			
ORGANISM	Arabidopsis thaliana			
DEFINITION	Arabidopsis; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1. (bases 1 to 70)			
AUTHORS	Barnache,F., Gaspin,C., Guyot,R. and Echeverria,M.			
TITLE	EXTENSIVE characterization of methylation guide small nucleolar RNAs in arabidopsis thaliana			
JOURNAL	Unpublished			
REFERENCE	2. (bases 1 to 70)			
AUTHORS	Barnache,F., Gaspin,C., Guyot,R. and Echeverria,M.			
TITLE	Direct Submission			
JOURNAL	Submitted (06-DHC-2000) Laboratoire Genome et Developpement des Plantes, Universite de Perpignan, UMR CNRS 5096, Avenue de Villeneuve, Perpignan, Pyrenees Orientales 66860, France			
FEATURES	source			
BASE COUNT	19 a 9 g 19 g 23 t			
ORIGIN	/organism="Arabidopsis thaliana"			
RESULT	15			
LOCUS	S45981	86 bp	RNA	linear
DEFINITION	Selenoprotein A [Clostridium purinolyticum, Genomic RNA, 86 nt].			
BASE COUNT	19 a 9 g 19 g 23 t			
ORIGIN	/db_xref="taxon:702"			
FEATURES	misc_RNA			
BASE COUNT	19 a 9 g 19 g 23 t			
ORIGIN	/organism="Arabidopsis thaliana"			
RESULT	1			
LOCUS	3764	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	3821			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
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RESULT	1			
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DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
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DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
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DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
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DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			
LOCUS	5	0.6%	Score 24.4; DB 8;	Length 70;
DEFINITION	Best Local Similarity 63.8%; Pred. No. 2.9e+05; Mismatches 37; Conservative 0; Indels 0; Gaps 0;			
BASE COUNT	62			
ORIGIN	/db_xref="taxon:32630"			
RESULT	1			

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on: August 13, 2002, 20:24:26 ; Search time 416.67 Seconds
(without alignments)
17034.402 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 cttaaaggatccccggatga.....tggtagagatattttc 4134
Scoring table: IDENTITY_NUC
GAPOP 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Minimum DB seq length: 15
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

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2: /SINSL/geodata/geneseq/geneseq -emb1/NA1981.DAT:*

3: /SINSL/geodata/geneseq/geneseq -emb1/NA1982.DAT:*

4: /SINSL/geodata/geneseq/geneseq -emb1/NA1983.DAT:*

5: /SINSL/geodata/geneseq/geneseq -emb1/NA1984.DAT:*

6: /SINSL/geodata/geneseq/geneseq -emb1/NA1985.DAT:*

7: /SINSL/geodata/geneseq/geneseq -emb1/NA1986.DAT:*

8: /SINSL/geodata/geneseq/geneseq -emb1/NA1987.DAT:*

9: /SINSL/geodata/geneseq/geneseq -emb1/NA1988.DAT:*

10: /SINSL/geodata/geneseq/geneseq -emb1/NA1989.DAT:*

11: /SINSL/geodata/geneseq/geneseq -emb1/NA1990.DAT:*

12: /SINSL/geodata/geneseq/geneseq -emb1/NA1991.DAT:*

13: /SINSL/geodata/geneseq/geneseq -emb1/NA1992.DAT:*

14: /SINSL/geodata/geneseq/geneseq -emb1/NA1993.DAT:*

15: /SINSL/geodata/geneseq/geneseq -emb1/NA1994.DAT:*

16: /SINSL/geodata/geneseq/geneseq -emb1/NA1995.DAT:*

17: /SINSL/geodata/geneseq/geneseq -emb1/NA1996.DAT:*

18: /SINSL/geodata/geneseq/geneseq -emb1/NA1997.DAT:*

19: /SINSL/geodata/geneseq/geneseq -emb1/NA1998.DAT:*

20: /SINSL/geodata/geneseq/geneseq -emb1/NA1999.DAT:*

21: /SINSL/geodata/geneseq/geneseq -emb1/NA2000.DAT:*

22: /SINSL/geodata/geneseq/geneseq -emb1/NA2001A.DAT:*

23: /SINSL/geodata/geneseq/geneseq -emb1/NA2001B.DAT:*

24: /SINSL/geodata/geneseq/geneseq -emb1/NA2002.DAT:*

RESULT 1
AAK51341/c
ID AAK51341 standard; DNA; 91 BP.
XX
AC AAK51341;
DT (06-NOV-2001) (first entry)
XX Human bone marrow expressed single exon probe SEQ ID NO: 25898.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PP 30-JAN-2001; 2001WO-US00668.
PP
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	91	2.2	91 22 ARK51341	Human bone marrow probe #26094 used
C 2	91	2.2	91 22 ARK513408	Human SNP oligonucleotide probe
C 3	50	1.2	51 22 ARK26826	Human Nr-CAM gene
C 4	48.8	1.2	60 21 ARK238172	Human Nr-CAM gene
C 5	38	0.9	38 21 ARK38153	Human Nr-CAM gene
C 6	28.8	0.7	97 21 ARK14618	Human secreted protein coding sequence
C 7	28	0.7	29 19 ARW40897	Probe used to isolate cDNA clone C
C 8	28	0.7	29 21 ARK5165	Human cDNA clone C
C 9	28	0.7	22 ARK98540	Human cDNA clone C

XX WPI; 2001-488900/53.

DR XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

XX PS Example 4; SEQ ID NO: 25898; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is one of

CC the probes of the invention.

XX SQ Sequence 91 BP; 24 A; 23 C; 23 G; 21 T; 0 other;

Query Match 2.2%; Score 91; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 atgcggaaaaaaagaagcgcttatctggggcgaggccctgttgcac 189
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 ATGCCGAAAGAAGACCGCTTCGGGAGATGCCCCATGTTCTTGCCAG 32
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 atgatttagtgcaactggaaagtgactctgtatcggagatgcctgttgcac 220
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 ATGATTAGTGTCACTGGAAAGTACTCTGTGATC 1
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 2
AA157408/C
ID AA157408 standard; DNA; 91 BP.
XX AC AA157408;
XX AC AA157408;
XX DT 17-OCT-2001 (first entry)
DE Probe #26094 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO20015272-A2.
XX PD 0-9-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 01-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0508408.
PR 03-AUG-2000; 2000US-0622366.
PR 21-SEP-2000; 2000US-0234687.
PR 04-OCT-2000; 2000GB-0024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PT Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX DR Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX CC The present invention relates to single exon nucleic acid probes useful for
PS Claim 25; SEQ ID NO 26094; 654pp; English.
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX SQ Sequence 91 BP; 24 A; 23 C; 23 G; 21 T; 0 other;

Query Match 2.2%; Score 91; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 atgcggaaaaaaagaagcgcttatctggggcgaggccctgttgcac 189
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 ATGCCGAAAGAAGACCGCTTCGGGAGATGCCCCATGTTCTTGCCAG 32
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 atgatttagtgcaactggaaagtgactctgtatcggagatgcctgttgcac 220
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 ATGATTAGTGTCACTGGAAAGTACTCTGTGATC 1
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 3
ID AAL26826 standard; DNA; 51 BP.
XX AC AAL26826;
XX DT 24-JAN-2002 (first entry)
DE Human SNP oligonucleotide #34.
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytokine; kinase; cytokine; interferon;
KW interleukin; G-Protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX OS Homo sapiens.
XX PN WO00147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX PS Claim 1; Page 149; 4143pp; English.

XX CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytokines, kinases, cytokines, interferons, interleukins,
CC protein coupled receptors and thioestersases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Graves' disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

Query Match	1.2%; Score 50; DB 22; Length 51;
Best Local Similarity	98.0%; Pred. No. 0.00014;
Matches	50; Conservative
Qy	1177 gtttaggttaaaggcgctccatctgtatcacagcccccacaaatcttg 1227
Db	1 gttagatgttaaaggcgctccatctggatcacagcccccacaaatcttg 51

RESULT 4
AAZ38172 standard; DNA; 60 BP.
ID AaZ38172
XX
AC AaZ38172;
XX

XX
XX
DE Human Nf-CAM gene fragment.

KW tumororigenesis; malignancy; cancer; leukaemia; hyperproliferative disorder;
KW degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
KW systemic lupus erythematosus; demyelinating disease; growth; human; ss.

OS
XX
PN
XX
DD
Homo sapiens.
WO9955380-A1.
01 - WO991 000

XX
PF 27-APR-1999; 99W0-US09039.
XX
PR 27-APR-1998; 98US-0083152.

XX
XX
PA
XX
PT
Murphy GP., Rovnton AF., Sehgal A.
(PACI-) PACIFIC NORTHWEST CANCER FOUND.

XX
DR
WPI; 2000-023268/02.
XX
PT
Use of neuron-glia-related cell adhesion molecule for developing agents
for
the
treatment
of
cancer

XX
PT
PS
Examples: Page 123; 183pp; English.
wounds -

The invention relates to the use of neuron-glia-related cell adhesion molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or preventing disorders involving cell proliferation. An antisense nucleic acid complementary to at least a portion of an RNA transcript of a Nr-CAM gene can be used to inhibit hyperproliferation of a tumor cell, for the treatment of tumorigens. Agents which inhibit and promote Nr-CAM function can be used for the treatment of various diseases and disorders (see AA38152 for a detailed description). The products can also be used for detection, diagnosis and production of animal models. The present sequence represents a human Nr-CAM gene fragment against which phosphorothioate oligonucleotides are designed.

Query Match 1.2%; Score 48.8; DB 21; Length 60;

CC horses, pigs, goats, deer, chickens) and plants (particularly edible
 CC plants, e.g. tomatoes, melons, lettuce, carrots, potatoes, and other
 CC vegetables), particularly those that are food or material sources. They
 can also be used in vitro e.g. to expand cells e.g. stem cells,
 CC progenitor cells, muscle cells, fibroblasts, or liver cells to grow
 cells/tissue in vitro prior to administration to a patient. The products
 can also be used for detection, diagnosis and production of animal
 models. The present sequence represents a previously cloned human Nr-CAM
 CC gene (accn no: AAU55258) fragment.
 XX sequence 38 BP; 12 A; 5 C; 7 G; 14 T; 0 other;

Query Match 0.9%; Score 38; DB 21; Length 38;
 best Local Similarity 100.0%; Pred. No. 0.4%;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 tctcatactatggtagagatatatttc 4134
 Db 1 tctcatactatggtagagatatatttc 38

RESULT 6
 AAC14618
 ID AAC14618 standard; cDNA; 97 BP.
 XX
 AC AAC14618;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 18693.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PR 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.

XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 18693; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX Sequence 97 BP; 43 A; 8 C; 28 G; 14 T; 4 other;

Query Match 0.7%; Score 28; DB 19; Length 29;
 best Local Similarity 96.6%; Pred. No. 3e+02;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3853 aaaaaggatgtgacacagctatgtactatggagaagggttaatggcagtcc 3912
 Db 21 atatggaaagaacaacaaagacagcccttgatgtatgaasmagatcttgc 80

QY 3913 atatggatg 3922
 Db 81 gatggatg 90

RESULT 7
 AAU40897/C
 ID AAU40897 standard; DNA; 29 BP.
 XX
 AC AAU40897;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Probe for coding sequence of clone C0722_1.
 XX
 KW Human; nutritional supplement; cell proliferation/differentiation;
 KW cytokine; immunostimulant; immunosuppressant; haemopoiesis regulator;
 KW receptor/ligand activity; cathein/tumour invasion suppressor; probe;
 KW anti-inflammatory; tumour inhibitor; clone C0722_1; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9824905-A2.
 XX
 PD 11-JUN-1998.
 XX
 PP 05-DEC-1997; 97WO-US22211.
 XX
 PR 03-DEC-1997; 97US-0984516.
 PR 06-DEC-1996; 96US-0762216.
 XX
 (GEMY) GENETICS INST INC.
 XX
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racine LA, Spaulding V, Treacy M;
 XX
 DR WPI; 1998-333324/29.
 XX
 PT New isolated polynucleotides encoding secreted polypeptides -
 PT isolated from a human foetal kidney cDNA library, a human adult
 PT blood cDNA library or a human adult brain cDNA library
 XX
 PS Disclosure; Page 93; 109pp; English.

This sequence represents a probe for the coding sequence of clone
 CC C0722_1 of the invention. The clone was isolated from a human adult
 CC brain cDNA library. The DNAs and proteins can be used as nutritional
 CC sources or supplements, or may exhibit cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haemopoiesis regulating activity, receptor/ligand activity,
 CC anti-inflammatory activity, cadherin/tumour invasion suppressor activity,
 CC tumour inhibition activity or other activities.
 XX Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;

Query Match 0.7%; Score 28; DB 19; Length 29;
 best Local Similarity 96.6%; Pred. No. 3e+02;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 75 aaggaaatcgatgtgatctcgac 103

Db	29 AAGGAATTTCAGTGCTCAGCNG 1
RESULT	8
AA64165/C	
ID	AA64165 standard; DNA; 29 BP.
XX	AA64165;
AC	
XX	20-DEC-2000 (first entry)
DE	Probe used to isolate cDNA encoding secreted protein clone C0722_1.
XX	Human; secreted protein; immune deficiency; infectious disease; tissue growth; wound healing; tissue repair; burn; incision; ulcer; osteoporosis; osteoarthritis; Periodontal disease; tooth repair; nervous system disorder; angiogenic activity; fibrosis; fertility; KW thrombolytic; coagulation disorder; antiinflammatory activity; KW inflammatory condition; probe; ss.
XX	OS Homo sapiens.
FH	Location/Qualifiers
FT	modified_base 2
FT	
FT	
XX	
PN	W020050592-A1.
XX	
PD	31-AUG-2000.
XX	
PP	24-FEB-2000; 2000WO-US04731.
XX	
PR	24-FEB-1999; 99US-0256938.
XX	
PA	(GEMY) GENETICS INST INC.
XX	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PT	Merberg D, Treacy M, Bowman MR, Spaulding V;
DR	WPI: 2000-558399/51.
XX	New secreted polypeptides and nucleic acids encoding them used for treating various anemias, bone, cartilage, tendon, ligament and/or nerve tissue or regeneration, contraceptives, and nutritional supplements -
XX	WPI: 2000-558399/51.
PS	Disclosure; Page 115; 119pp; English.
XX	The present sequence represents a probe for cDNA encoding a human secreted protein. The polypeptides may be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The polypeptides are also used in compositions for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers. The protein is used in the treatment of osteoporosis or osteoarthritis, periodontal disease and other tooth repair processes, and nervous system disorders. They also exhibit angiogenic activity and protect, regenerate and treat lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They promote or inhibit tissue differentiation and are used as contraceptives and to enhance fertility. They also have a hemostatic or thrombolytic activity and can be used to treat various coagulation disorders. They also have an antiinflammatory activity and can be used to treat inflammatory conditions.
CC	Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;
CC	Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;
CC	Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;
XX	
Qy	Best Local Similarity 95.6%; Pred. No. 3e+02; 0; Mismatches 1; Indels 0; Gaps 0;
DB	29 AAGGAATTTCAGTGCTCAGCNG 1
RESULT	9
AAF8540/C	
ID	AAF8540 standard; DNA; 29 BP.
XX	AAF8540;
AC	
XX	07-JUN-2001 (first entry)
DE	Human cDNA clone C0722_1 specific probe SEQ ID 250.
XX	Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss; haemopoiesis; probe.
XX	OS Homo sapiens.
XX	W020119988-A1.
XX	
PD	22-MAR-2001.
XX	
PF	14-SEP-2000; 2000WO-US25135.
XX	
PR	17-SEP-1999; 99US-0398829.
XX	
PA	(GEMY) GENETICS INST INC.
XX	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI	Merberg D, Treacy M, Bowman MR, Spaulding V;
DR	WPI; 2001-244801/25.
XX	Isolated nucleic acids encoding polypeptides, useful for modulating immune system and hematopoiesis regulating activity -
PT	e.g. cytokine and cell proliferation/differentiation activity -
PS	Disclosure; Page 540; 557pp; English.
XX	Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB9067 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, their agonists and/or antagonists exhibit hematopoiesis, regulating activity; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; haemopoiesis activity; adhesion/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF9490 - AAF98572 which are specific for the cDNA clones encoding the secreted proteins.
XX	Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;
SQ	Best Local Similarity 96.6%; Pred. No. 3e+02; Length 29; Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	75 aaggaaatttcagtgtgactcagcag 103
DB	29 AAGGAATTTCAGTGCTCAGCNG 1

RESULT 10
DE AA238180/C
ID AA238180 standard; DNA; 50 BP.
XX AC AA238180;
XX DT 14-FEB-2000 (first entry)
XX DE Human Nr-CAM gene specific primer Br307.
XX KW Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation; tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder; degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes; systemic lupus erythematosus; demyelinating disease; PCR primer; ss. OS Synthetic.
OS Homo sapiens.
XX PN WO9955380-A1.
XX PD 04-NOV-1999.
XX PR 27-APR-1999; 99WO-US09039.
XX PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.
XX PI Murphy GP, Baynton AL, Sehgal A;
XX DR WPI; 2000-023268/02.
XX PT Use of neuron-glia-related cell adhesion molecule for developing agents for the diagnosis and treatment of e.g. cancers, hyperproliferative disorders, growth deficiencies, degenerative disorders, trauma or wounds -
XX PS Examples; Page 124; 183pp; English.
XX CC The invention relates to the use of neuron-glia-related cell adhesion molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or preventing disorders involving cell proliferation. An antisense nucleic acid complementary to at least a portion of an RNA transcript of a NR-CAM gene can be used to inhibit hyperproliferation of a tumor cell, for the treatment of tumorigenesis. Agents which inhibit and promote Nr-CAM function can be used for the treatment of various diseases and disorders (see AA238152 for a detailed description). The products can also be used for detection, diagnosis and production of animal models. Sequences AA238179-80 represent primers specific for the human Nr-CAM gene.
XX SQ Sequence 50 BP; 15 A; 11 C; 11 G; 13 T; 0 other;

Query Match Best Local Similarity 0.6%; Score 26; DB 21; Length 50; Matches 30; conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1399 gttatctatgtggcaatgtgcataatgaaatggat 1434
Db 50 GTATGGGATCCCAATGCTCTAATGAAATGGAT 15

RESULT 11
ID AAT44495/C
XX AC AAT44495;
XX DT 22-FEB-1997 (first entry)

Murine p57KIP2 gene translation initiation region.
DE XX Cyclin-dependent kinase inhibitor; CDK; CDI; P57KIP2; cell cycle; cancer; hyperplasia; ulcer; hyperproliferation; hypoproliferation; diagnosis; gene therapy; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
FT exon 1..15
FT /tag= a
FT /note= "3' end of exon sequence"
FT intron 16..28
FT /*tag= b
FT /note= "base n at position 22 denotes an approx. 200 bp intronic sequence not provided in Fig 4"
FT exon 29..82
FT /*tag= c
FT /codon_start= 39
FT /note= "there is an alternative codon start site at position 78 for use with B and B'"
FT misc_feature 29
FT /*tag= d
FT /label= A
FT /note= "p57 acceptor site A"
FT misc_feature 67
FT /*tag= e
FT /label= B
FT /note= "alternative acceptor site B"
FT misc_feature 70
FT /*tag= f
FT /note= "alternative acceptor site B'"
FT misc_feature 70
FT /*tag= B'
FT /note= "alternative acceptor site B'"
PN WO9631134-A1.
XX PD 10-OCT-1996.
XX PR 03-APR-1995; 95US-0415655.
XX PA (SIOK) SLOAN KETTERING INST CANCER RES.
XX Lee M, Massague J;
XX DR WPI; 1996-16497146.
XX P-PSDB; AAW01438.

PT Mammalian p57-KIP2 and related DNA - used to develop prods. useful for diagnosis and treatment of hyper- and hypo-proliferative disorders
XX Disclosure; Fig 4; 98pp; English.

3 Distinct cDNA clones (AAT44496-98) are derived from genomic DNA (AAT44495) in the translation start region of the murine gene (see also AAT44494) coding for cyclin-dependent kinase inhibitor p57KIP2 (AAW01477). These result from splicing at position A, leading to the full-length (349-amino acid) protein having the N-terminal sequence shown in AAW01438, or alternative splicing at positions B or B', resulting in a 335-amino acid product, designated p57KIP2B. The intron sequence in the genomic DNA was identified by PCR analysis (see also AAT4500-01).

XX SQ Sequence 82 BP; 21 A; 27 C; 21 G; 12 T; 1 other;

Query Match Best Local Similarity 0.6%; Score 26; DB 17; Length 82; Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

age 9

us-09-301-380-1.rng

ug 14 08:10:40 2002

search completed: August 13, 2002, 22:49:51
search time 8725 sec
Job time

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Gencore version 4.5
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Om nucleic - nucleic search, using sw model

Run on:

August 13, 2002, 19:38:44 ; Search time 82.1 seconds

{without alignments)

12368.440 Million cell updates/sec

title:

US-09-301-380-1

perfect score:

4134 cttcaaaatcccccgtatgatggtagagatatatcc 4134

sequence:

IDENTY.NUC

scoring table:

Gapop 10.0 , Gapext 1.0

searched:

38353 seqs, 122816752 residues

total number of hits satisfying chosen parameters:

576162

post-processing:

Minimum DB seq length: 15

maximum DB seq length: 100

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 2: /cggn2_6/ptodata/1/ina/5B_COMB.seq: *
 3: /cggn2_6/ptodata/1/ina/6A_COMB.seq: *
 4: /cggn2_6/ptodata/1/ina/6B_COMB.seq: *
 5: /cggn2_6/ptodata/1/ina/PCRTUS_COMB.seq: *
 6: /cggn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
US-08-441-430-9
Sequence 9, Application US/08441430
Patent No. 5601942
GENERAL INFORMATION:
APPLICANT: Buchwald, Manuel
APPLICANT: Strathdee, Craig A.
APPLICANT: Wevrick, Rachel
APPLICANT: Matthew, Christopher George Porter
TITLE OF INVENTION: Fanconi Anemia Type C Gene
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh &
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.

ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: DISK, 3+inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORDPERFECT 5.1/ASCII Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,430
FILING DATE: May 15, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/876,285
FILING DATE: April 29, 1992
APPLICATION NUMBER: U.S. 07/918,313
FILING DATE: July 21, 1992
APPLICATION NUMBER: U.S. 08/003,963
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 3812-42824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: Nucleic Acid
STRANDNESS: Double stranded
TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA

c 28 22.2 0.5 79 4 US-08-460-736-158 Sequence 158, APP
c 29 22.2 0.5 84 1 US-08-182-175A-27 Sequence 27, Appl
c 30 22.2 0.5 84 1 US-08-474-633N-68 Sequence 68, Appl
c 31 22.2 0.5 84 5 PCT-US92-06412-27 Sequence 27, Appl
c 32 22.2 0.5 95 2 US-08-332-766A-41 Sequence 41, Appl
c 33 22 0.5 60 1 US-08-153-848-10 Sequence 10, Appl
c 34 22 0.5 60 3 US-09-299-843A-10 Sequence 10, Appl
c 35 22 0.5 60 4 US-09-088-337B-10 Sequence 10, Appl
c 36 22 0.5 90 1 US-08-513-846-2 Sequence 2, Appl
c 37 22 0.5 90 1 US-08-513-846-18 Sequence 18, Appl
c 38 22 0.5 93 2 US-08-105-989-12 Sequence 12, Appl
c 39 22 0.5 93 3 US-09-138-922-12 Sequence 25, Appl
c 40 22 0.5 56 1 US-08-441-430-25 Sequence 22, Appl
c 41 21.8 0.5 76 3 US-08-284-516-22 Sequence 42, Appl
c 42 21.8 0.5 81 1 US-08-238-863-42 Sequence 42, Appl
c 43 21.8 0.5 81 1 US-08-441-407-42 Sequence 185, Appl
c 44 21.8 0.5 81 5 PCT-US95-05600-186 Sequence 185, Appl

Result No.	Score	Query Match	Length	DB ID	Description
1	25	0.6	70	1 US-08-441-430-9	Sequence 9, Appl
c 2	24	0.6	100	4 US-09-554-805-23	Sequence 23, Appl
c 3	23.5	0.6	67	4 US-09-035-768B-83	Sequence 83, Appl
c 4	23.4	0.6	66	2 US-08-709-877A-15	Sequence 15, Appl
c 5	23.4	0.6	66	4 US-09-104-382-15	Sequence 15, Appl
c 6	23	0.6	60	3 US-08-415-655-10	Sequence 10, Appl
c 7	22.8	0.6	63	1 US-08-366-499-1	Sequence 1, Appl
c 8	22.8	0.6	63	5 PCT-US91-02311-1	Sequence 1, Appl
c 9	22.8	0.6	78	1 US-08-446-102-1	Sequence 1, Appl
c 10	22.8	0.6	78	1 US-08-446-102-2	Sequence 2, Appl
c 11	22.8	0.6	78	4 US-08-617-010C-15	Sequence 15, Appl
c 12	22.8	0.6	78	4 US-08-566-591-15	Sequence 15, Appl
c 13	22.8	0.6	100	4 US-09-242-690A-58	Sequence 58, Appl
c 14	22.6	0.5	94	1 US-08-105-483-447	Sequence 447, Appl
c 15	22.6	0.5	94	1 US-08-105-483-448	Sequence 448, Appl
c 16	22.5	0.5	94	1 US-08-709-203-447	Sequence 447, Appl
c 17	22.5	0.5	94	1 US-08-039-205-448	Sequence 448, Appl
c 18	22.5	0.5	94	1 US-08-033-275-159	Sequence 159, Appl
c 19	22.5	0.5	94	1 US-08-303-275-160	Sequence 160, Appl
c 20	22.5	0.5	94	1 US-08-158-101-447	Sequence 447, Appl
c 21	22.5	0.5	94	1 US-08-158-101-448	Sequence 448, Appl
c 22	22.5	0.5	100	3 US-08-936-561-61	Sequence 61, Appl
c 23	22.4	0.5	78	4 US-09-240-078-43	Sequence 43, Appl
c 24	22.2	0.5	77	1 US-08-242-663A-3	Sequence 3, Appl
c 25	22.2	0.5	77	5 PCT-US95-06132-3	Sequence 158, Appl
c 26	22.2	0.5	79	2 US-08-184-009-158	Sequence 158, Appl
c 27	22.2	0.5	79	2 US-08-458-336-158	Sequence 158, Appl

HYPOTHETICAL: NO
 ANTI-SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-441-430-9

Query Match 0.6%; Score 25; DB 1; Length 70;
 Best Local Similarity 61.5%; Pred. No. 5.2e+02;
 Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 3449 aaatgttaatggttccggatctttggtaaaggcttaatgcccggaaacgcat 3508
 Db 4 AGAGAGTTAATCTGCTGCACTTCTTGATTAAATGGATTAAAGTGCCTGCTT 63
 QY 3509 acaa 3513
 Db 64 AAAAA 68

RESULT 2
 US-09-564-805-23/C
 ; Sequence 23, Application US/09564805
 ; GENERAL INFORMATION:
 APPLICANT: Tavtigian, Sean V.
 APPLICANT: Teng, David H.F.
 APPLICANT: Simard, Jacques
 APPLICANT: Rommens, Johanna M.
 APPLICANT: Myriad Genetics, Inc.
 TITLE OF INVENTION: chromosome 17p-Linked Prostate Cancer Susceptibility
 TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
 FILE REFERENCE: 2318-258
 CURRENT APPLICATION NUMBER: US/09/564,805
 CURRENT FILING DATE: 2000-05-05
 PRIOR APPLICATION NUMBER: US 60/107,468
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: 09/434,382
 PRIOR FILING DATE: 1999-11-05
 NUMBER OF SEQ ID NOS: 240
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 23
 LENGTH: 100
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(100)
 OTHER INFORMATION: exon 20
 ; US-09-564-805-23

Query Match 0.6%; Score 24; DB 4; Length 100;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 48; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 3297 caaagtcaactgttaataccaggatcagcaatctttactgtcgactgtcgagaccta 3356
 Db 94 CAAATACATGTGCAACAGCGAACUGATCATCTTCAGTGCAAGCTGGACGARCTC 35
 QY 3357 tgccaaatccgttgaaatggatgg 3384
 Db 34 AGCCCCCTCCCTGAGGCGATTCGGACGAGC 7

RESULT 4
 US-08-709-874A-15
 ; Sequence 15, Application US/08709874A
 ; Patent No. 5854040
 ; GENERAL INFORMATION:
 APPLICANT: Ozaki, Akio
 APPLICANT: Mori, Hideo
 APPLICANT: Shibusai, Takeshi
 APPLICANT: Ando, Katsuhiko
 APPLICANT: Chiba, Shigeru
 TITLE OF INVENTION: Process for Producing
 TITLE OF INVENTION: trans-4-Hydroxy-L-Proline
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS, LLP
 STREET: 1300 NORTH SEVENTEENTH STREET
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22209
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Query Match 0.6%; Score 25; DB 1; Length 70;
 Best Local Similarity 76.3%; Pred. No. 1.3e+03;
 Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1228 ctgtcccccaaggaggatggacccatgttcgcggcgg 1265
 Db 39 CTGCTCCGGGGAACGTGGACCCCTGAGCTCAGAGC 2

RESULT 3
 US-09-025-769B-83/C
 ; Sequence 83, Application US/09025769B
 ; Patent No. 630064
 ; GENERAL INFORMATION:
 APPLICANT: Knapik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,874A
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/301,653
 FILING DATE: 07-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: TERRY, DAVID T.
 REGISTRATION NUMBER: 20178
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-312-6600
 TELEFAX: 703-312-6666
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 66 base pairs
 STRANDEDNESS: single
 TYPE: nucleic acid
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid, synthetic DNA
 US-08-709-874A-15

Query Match 0.6%; Score 23.4; DB 2; Length 66;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 Qy 3266 ctgtatcttcacctgtatggcgccaaatgttcaatccaggatca 3325
 Db 1 CCGGAATTCGTCGACTTCACGGGCCAGGCCATCTTCAATCAGCAGATAAGCCGCTTC 60
 Qy 3326 gcaat 3330
 Db 61 ACGAT 65

RESULT 5 US-09-104-382-15
 Sequence 15, Application US/09104382
 Patent No. 624231
 GENERAL INFORMATION:
 APPLICANT: Ozaki, Aki
 APPLICANT: Mori, Hideo
 APPLICANT: Shibasaki, Takeshi
 APPLICANT: Ando, Katsuiko
 APPLICANT: Chiba, Shigeru
 TITLE OF INVENTION: Process for Producing
 TITLE OF INVENTION: Trans-4-Hydroxy-L-Proline
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS, LLP
 STREET: 1100 NORTH SEVENTEENTH STREET
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22209

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/415,655
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 1747/47418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 10:

APPLICATION NUMBER: 08/709,874
 FILING DATE: 09-SEP-1996
 APPLICATION NUMBER: 08/301,653
 FILING DATE: 07-SEP-1994
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/482,554
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Terry, David T.
 REGISTRATION NUMBER: 20178
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-312-6600
 TELEFAX: 703-312-6666
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 66 base pairs
 STRANDEDNESS: single
 TYPE: nucleic acid
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid, synthetic DNA
 US-09-104-382-15

Query Match 0.6%; Score 23.4; DB 4; Length 66;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 Qy 3266 ctgtatcttcacctgtatggcgccaaatgttcaatccaggatca 3325
 Db 1 CCGGAATTCGTCGACTTCACGGGCCAGGCCATCTTCAATCAGCAGATAAGCCGCTTC 60
 Qy 3326 gcaat 3330
 Db 61 ACGAT 65

RESULT 6 US-08-415-655-10/C
 Sequence 10, Application US/08415655
 Patent No. 6025480
 GENERAL INFORMATION:
 APPLICANT: Massague, Joan
 APPLICANT: Lee, Mong-hong
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
 TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
 TITLE OF INVENTION: SAME
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10035

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/415,655
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 1747/47418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 10:

TITLE OF INVENTION: NUCLEIC ACID DETECTION METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, I.L.P.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,102
FILING DATE: 19-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 16865.0199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
8-446-102-1

Primary Match Score 22.8; DB 1; Length 0.6%;
Sequence 2, Application US/08446102
at Local Similarity 59.1%; Pred. No. 2.5e+03;
Matches 39; Conservative 0; Mismatches 27; In
GENERAL INFORMATION:
69 CCAGGGATTCGGT-TAGCTGACTGCTGCAGCTGCAGCTGG
2054 caaatc 2059
9 CAGATC 4

BLT 10

Sequence 2, Application US/08446102
Patent No. 5753439

APPLICANT: SMITH, Cassandra L.
APPLICANT: YAAR, Ron
APPLICANT: SZAFRANSKI, Przemyslaw
APPLICANT: CANTOR, Charles R.
TITLE OF INVENTION: NUCLEIC ACID DETECTION METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, I.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20004-2400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,102
 FILING DATE: 19-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Remenick, James
 REGISTRATION NUMBER: 36,902
 REFERENCE/DOCKET NUMBER: 16865.0199
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-639-7700
 TELEFAX: 202-639-7890
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 08-446-102-2

Start	End	Sequence	Score	DB	Length	Match
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0	1	CGAGGATTCTGGTTAGGGTGACTGTCTGCCTCTGGATGATCCGACCAT	69	1	78	0.6%; Pred. No. 2.5e+03; Mismatches 27; Indels 0; Gaps 0;
0	1	CGAGGATTCTGGTTAGGGTGACTGTCTGCCTCTGGATGATCCGACCAT	69	1	78	Sequence 15, Application US/0861701C
0	1	CGAGGATTCTGGTTAGGGTGACTGTCTGCCTCTGGATGATCCGACCAT	69	1	78	Patent No. 6191144
GENERAL INFORMATION:						
APPLICANT: Hubert K ster						
TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY						
NUMBER OF SEQUENCES: 21						
CORRESPONDENCE ADDRESS:						
ADDRESSEE: Heller Elrman White & McAuliffe						
STREET: 4250 Executive Square, 7th Floor						
CITY: La Jolla						
STATE: CA						
COUNTRY: USA						
ZIP: 92037-9103						
COMPUTER READABLE FORM:						
MEDIUM TYPE: Diskette						
COMPUTER: IBM Compatible						
OPERATING SYSTEM: DOS						
SOFTWARE: ASCII						
CURRENT APPLICATION DATA:						
APPLICATION NUMBER: US/08/617,010C						
FILING DATE: 18-MAR-1996						
CLASSIFICATION: 435						
PRIOR APPLICATION DATA:						

TITLE OF INVENTION: STRAIN
 NUMBER OF SEQUENCES: 462
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,483
 APPLICATION NUMBER: 07/847,951
 FILING DATE: 12-AUG-1993
 PRIORITY NUMBER: US 07/847,951
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REFERENCE/DOCKET NUMBER: 25,506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 448:
 LENGTH: 94 base pairs
 SEQUENCE CHARACTERISTICS:
 LENGTH: 94 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ;US-08-105-483-448

RESULT 15
 US-08-105-483-448/C
 ; Sequence 448, Application US/08105483
 ; Patent No. 5494807
 GENERAL INFORMATION:
 APPLICANT: Paoletti, Enzo
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 NUMBER OF SEQUENCES: 462
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

Query Match 0.5%; Score 22.6; DB 1; Length 94;
 Best local Similarity 54.1%; Pred. No. 3.2e+03;
 Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
 Qy 619 cccccaatggatttacccacccataatattttggatgatataatcccttcggactt 678
 Db 4 CCRCCTTTAGAACACCGAGATATTTCCTTGTGGGATCAACTTAAACCTCCT 63
 Qy 679 ccacaaggagggatctcaag 703
 Db 31 TTAGAAAAGTAGATAATTGAG 7
 Db 64 TTTAGAAAGATAGATAATTGAG 88

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,483
 FILING DATE: 12-AUG-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/847,951
 FILING DATE: 06-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REFERENCE/DOCKET NUMBER: 25,506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 448:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 94 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ;US-08-105-483-448

Query Match 0.5%; Score 22.6; DB 1; Length 94;
 Best local Similarity 54.1%; Pred. No. 3.2e+03;
 Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
 Qy 619 cccccaatggatttacccacccataatattttggatgatataatcccttcggactt 678
 Db 91 CCRCCTTTAGAACACCGAGATATTTCCTTGTGGGATCAACTTAAACCTCCT 32
 Qy 679 ccacaaggagggatctcaag 703
 Db 31 TTAGAAAAGTAGATAATTGAG 7

Search completed: August 13, 2002, 22:42:33
 Job time: 11029 sec

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adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W." NBHL21. EST

BASE COUNT

16 a
21 c25 g
23 t

ORIGIN

AUTHORS Hall,N., Bowman,S., Lenard,N.J., Boggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nelsanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU27/4 Gurtat 10.1) was mechanically sheared to give a tight size distribution (~4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayer@tigr.org

Details of *T. brucei* sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucel/.

FEATURES

Source

1. .83 /organism="trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="293d12"

BASE COUNT

21 a	18 c	7 g	37 t
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ORIGIN

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Qy 1349 tagatgcgataccattttttcaaatgttcaagaaagtcacggcgtatata 1405
Db 83 TAGGTRAGTCACATTTTTTGAAAGAAAAAGAGGAGANATGCA 26

RESULT 7

AA470870/c AA470870 92 bp mRNA linear EST 14-AUG-1997 LOCUS neli903.s1 NCI_CGAP_Co3 Homo sapiens CDNA clone IMAGE:881716 3' DEFINITION similar to qb566915.cds1 ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.

ACCESSION AA470870 VERSION AA470870.1 GI:2198179

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 92) NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: crapbs@email.nih.gov

JOURNAL Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIN at: www.ncbi.nlm.nih.gov/bbfp/image/image.html

Seq primer: -41ml3 fwd. B7 from Amersham

High quality sequence stop: 1.

Location/Qualifiers 1. .92 /organism="Homo sapiens" /db_xref="taxon:9606"

FEATURES

Source

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Qy 1268 atggacacccaaaccagaataggtaggttcaacaatgggtccaaatggaaatggcc 1327
Db 80 ATTCGACCCCTAACGCCCGCTGCTCTCACAAAAGGAGTGGATATCT 21

RESULT 8

BG796297/c BG796297 93 bp mRNA linear EST 16-MAY-2001 LOCUS UTSW_SM1H9 UTSW_Aquilt Mouse Skeletal Muscle Library Mus musculus DEFINITION UTSW_SM1H9 mRNA sequence.

ACCESSION BG796297

VERSION BG796297.1 GI:14131867

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 93) Gaillard,T.D., Schageman,J.J., Pertsemidis,A., Garner,H.R., Williams,R.S. and Shonet,R.V.

AUTHORS UT Southwestern Medical Center, Adult Mouse Skeletal Muscle CDNA Library

TITLE Unpublished (2001)

COMMENT Contact: Schageman, JJ
Shonet/Garner Labs
University of Texas Southwestern Medical Center
6000 Harry Hines Blvd., NA2.225, Dallas, TX 75390, USA
Tel: 214 648 1674
Email: Jeff.Schageman@utsouthwestern.edu

CDNA library constructed by UTSW as a component of the Program for Genomic Applications (PGA) and the Reynolds Heart Disease Prevention grants for use in CDNA microarray experiments. Sequence Quality: Sequence ends were trimmed based on Percentage of ambiguous base calls or 'N's in windowed segments. Sequencing: First-pass sequencing; ABI Prism 377 sequencer and analysis software.

Seq primer: M13/pUC Reverse.

Location/Qualifiers

FEATURES source

1. .93 /organism="Mus musculus" /db_xref="taxon:10090"
/clone="UTSW_SM41H9"
/clone_id="UTSW_Adult Mouse Skeletal Muscle Library"
/sex="pooled"
/tissue_type="Diaphragm/Rhind limb muscles"
/cell_type="Skeletal muscle"
/dev_stage="2 months"
/lab_host="DH5a"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally."

		FAX: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0102 row: K column: 08 Seq primer: CGTGTAAAGGACGGCCAGT Class: plasmid ends
FEATURES	source	High quality sequence stop: 71. Location/Qualifiers
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BASE COUNT	17 a	10 c 17 g 27 t
ORIGIN		
		Query Match 0.6%; Score 25.8; DB 12; Length 71; Best Local Similarity 60.9%; Pred. No. 5e+04; Mismatches 42; Conservative 0; Indels 0; Gaps 0;
Matches		
Oy	2385	tcaagacctgataattggagatccgttgcgaatctatagg 2445
Db	3	TTAGTCGATGCTGATCATGGCAATTCAATTTGAATCTGTGAG 62
Oy	2446	ccaaaggctt 2454
Db	63	GCCCTGATTT 71
RESULT	14	
LOCUS	BE289162	85 bp mRNA
DEFINITION	601092758FL NCI_CCAP_Man5	Mus musculus
ACCESSION	BE289162	CDNA clone IMAGE:3487430
VERSION	BE289162.1	GI:9169349
KEYWORDS	EST.	
SOURCE		House mouse.
ORGANISM		Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 85)	NIH-MGC http://mgc.ncbi.nih.gov/ .
AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL		Unpublished (1999)
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapbsr@mail.nih.gov
		Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
		CDNA Library Preparation: Life Technologies, Inc.
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
FEATURES	source	DNA Sequencing by: Invitro Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL8525 row: c column: 15
	1. .85	High quality sequence stop: 85. Location/Qualifiers
		/organism="Mus musculus" /strain="C57/B6" /db_xref="taxon:10090" /clone="IMAGE:3487430" /clone_1ib="NCI_CGAP_Mam5" /tissue_type="tumor, gross tissue" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPOR6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT	35 a	10 c 22 g 18 t
ORIGIN		
		Query Match 0.6%; Score 25.8; DB 10; Length 85; Best Local Similarity 63.9%; Pred. No. 5.5e+04; Mismatches 39; Conservative 0; Indels 0; Gaps 0;
Matches		
Oy	3410	aatatcggtgtcgaggcggcaagaagaatgtggtaatggttctcgaa 3469
Db	5	AAAGGCCGAAGGAAGCTGCAGCAGATGTTGAANAGAANAAAATTCCTGTTGA 64
Oy	3470	9 3470
Db	65	6 65
RESULT	15	
LOCUS	FR0022001	99 bp DNA
DEFINITION	F.rubripes	linear GSS 10-DEC-1997
ACCESSION	AL014872	GSS sequence, clone 070116ae2, genomic survey sequence.
VERSION	AL014872.1	GT:2681240
KEYWORDS		GSS; genome survey sequence.
SOURCE		Takifugu rubripes.
ORGANISM		Takifugu rubripes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
REFERENCE		Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.
AUTHORS		Direct Submission
TITLE		Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmmp.mrc.ac.uk
JOURNAL		Vector: phblue-script II KS
COMMENT		V-type: phagemid
		PRIMER: KS
DESCR:		One pass dye-terminator sequencing of cosmid cloned genomic sequence.
FEATURES	source	Location/Qualifiers
	1. .99	/organism="Takifugu rubripes" /db_xref="taxon:31033" /clone_1ib="cosmid 070116" /clone="070116ae2"
BASE COUNT	24 a	26 c 23 g 24 t 2 others
ORIGIN		

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Query Match          0.6%; Score 25.8; DB 12; Length 99;
Best Local Similarity 57.0%; Pred. No. 6e+04; Mismatches 0;
Matches 45; Conservative 0; Indels 0; Gaps 0;
Oy 1905 caaggatcaactaggtggatgtatgtcgatgcacgatcggccatcacgttgtgt 1964
Db 16 CAATGGAACCCCTGGCTAGATCTGTCAAANCAGAGGATCTGGGACTACACATGCNC 75
Oy 1965 ggccaaacaccatctggac 1983
Db 76 TGCCACCAACACTCTGGC 94

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Job time: 6465 sec